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(54) Title: PNEUMOLYSIN MUTANTS AND PNEUMOCOCCAL VACCINES MADE THEREFROM (57) Abstract Mutants of pneumolysin that are non-toxic by reason of amino acid substitutions have been constructed. These mutants elicit an immune response in animals that is reactive to wild-type pneumolysin. The invention also encompasses vaccines for humans based on these mutants, including vaccines comprising conjugates with pneumococcal capsular polysaccharides.		

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PNEUMOLYSIN MUTANTS AND PNEUMOCOCCAL VACCINES
MADE THEREFROM

5 This invention relates to mutants of the toxin pneumolysin and pneumococcal vaccines based on these mutants.

BACKGROUND

10 *Streptococcus pneumoniae* (pneumococcus) is an important pathogen, causing invasive diseases such as pneumonia, meningitis and bacteraemia. Even in regions where effective antibiotic therapy is freely available, the mortality rate from pneumococcal pneumonia can be as high as 19% in hospitalized patients and this increases to 30-40% in patients with bacteraemia. These high mortality rates have been reported in the U.S.A. where pneumonia, of which *S. pneumoniae* is the commonest cause, is the fifth ranking cause of death. Indeed, pneumonia is the only infectious disease amongst the top ten causes of death in that country. In the United States mortality rates for pneumococcal meningitis range from 13-45%. In developing countries, in excess of 3 million children under the age of 5 years die each year from pneumonia, and again *S. pneumoniae* is the commonest causative agent. *S. pneumoniae* also causes less serious, but highly prevalent infections such as otitis media and sinusitis, which have a significant impact on health-care costs in developed countries. Otitis media is especially important in young children; sinusitis affects both children and adults.

25 In the late 1970's, a vaccine was licensed for the purpose of preventing serious infections, especially bacterial pneumonia and for protecting certain groups, such as splenectomized individuals and young children, who are particularly susceptible to fulminating pneumococcal disease. The vaccine is composed of purified capsular polysaccharides, which are the predominant pneumococcal surface antigens. However, each serotype of *S. pneumoniae* (of which there are 83) has a structurally distinct capsular polysaccharide, and immunization with one serotype confers no protection whatsoever against the vast majority of the others. The vaccine currently licensed in Australia contains polysaccharides purified from the 23 most common serotypes, which account for approximately 90% of pneumococcal infections in this country.

Protection even against those serotypes contained in the vaccine is by no means complete, and there have been several reports of serious, even fatal infections occurring in vaccinated high-risk individuals. The efficacy of the vaccine is poorest in young children, and several studies, including one conducted in Adelaide, have shown that the existing formulation has little or no demonstrable clinical benefit in this group. This apparent failure of the vaccine appears to be related to the poor immunogenicity of certain pneumococcal polysaccharides in children under 5 years of age. We have shown that the antibody response is particularly poor to the five serotypes which most commonly cause disease in children (types 6, 14, 18, 19 and 23). Indeed, the antibody response to these pneumococcal polysaccharides only approaches adult levels in children over 8 years of age at the time of vaccination.

In view of this, a vaccine, including antigens other than the capsular polysaccharides seems to be required to protect young children from pneumococcal infection. One such antigen could be pneumolysin, a protein toxin produced by all virulent *S. pneumoniae* isolates. Immunization of mice with this protein has been found to confer a degree of protection from pneumococcal infection.

However there is a difficulty in that pneumolysin is toxic to humans. Thus pneumolysin included in a vaccine must therefore be substantially non-toxic. However, the rendering of a pneumolysin non-toxic by most currently employed methods would be likely to alter the basic configuration of the protein so as to be immunogenically distinct from the native or wild-type pneumolysin. An immune response elicited by an altered protein that is immunogenically distinct from the native pneumolysin will have a decreased protective capacity or no protective capacity. Thus the difficulty is to produce an altered pneumolysin that is non-toxic and at the same time sufficiently immunogenically similar to the toxic form to elicit a protective immune response.

An altered pneumolysin with the above characteristics can then be used in a number of ways in a vaccine. Thus the altered pneumolysin may be used by itself to immunise, or alternatively the altered pneumolysin may be conjugated to pneumococcal polysaccharide, or

alternatively may be included in a vaccine wherein pneumococcal polysaccharides may be conjugated to another protein and the altered pneumolysin is present in a non-conjugated form only. Alternatively, pneumococcal polysaccharide and pneumolysin may both be used in an unconjugated form.

DESCRIPTION OF INVENTION

In a broad form therefore the invention may be said to reside in an altered pneumolysin being substantially non-toxic and being capable of eliciting an immune response in an animal being reactive to wild-type pneumolysin.

Preferably the altered pneumolysin has reduced complement binding activity as compared to wild-type pneumolysin. Reduction in the complement binding activity results in less inflammation at the site of administering the vaccine.

Preferably the altered pneumolysin has reduced Fc binding activity as compared to wild-type pneumolysin. Reduction in the Fc binding activity results in less inflammation at the site of administering the vaccine.

Preferably the altered pneumolysin is altered by reason of one or more amino acid substitutions relative to wild-type pneumolysin.

The pneumolysin may be altered in that the amino acid present at any one or more than one of residue sites 367, 384, 385, 428, 433 or 435 of wild-type pneumolysin are replaced, removed or blocked.

In a further form the invention could be said to reside in a vaccine including an altered pneumolysin, said altered pneumolysin being non-toxic and being capable of eliciting an immune response in an animal being reactive to wild-type pneumolysin.

Preferably the vaccine comprises capsular polysaccharide material conjugated with the altered pneumolysin.

The capsular material may be derived from any one or more of the *Streptococcus pneumoniae* serotypes 6A, 6B, 14, 18C, 19A, 19F, 23F, 1, 2, 3, 4, 5, 7F, 8, 9N, 9V, 10A, 11A, 12F, 15B, 17F, 20, 22F and 33F.

- 5 In this embodiment serotypes which are commonly associated with disease in children, and to which children generally have a poor immune response, may be specifically targeted (i.e. Danish serotypes 6A, 6B, 14, 18C, 19A, 19F and 23F). Other common serotypes contained in the present 23-valent Merck Sharp and Dohme vaccine
- 10 (Pneumovax 23) however, could also be used to synthesize conjugates (i.e. types 1, 2, 3, 4, 5, 7F, 8, 9N, 9V, 10A, 11A, 12F, 15B, 17F, 20, 22F and 33F) or indeed any other serotype. Conjugation of any pneumococcal polysaccharides to the protein carrier ensures good T-cell dependent immunogenicity in children, such that protective levels
- 15 of anti-polysaccharide antibody are produced.

- The combination of the altered pneumolysin together with the capsular material will ensure an extra degree of protection, particularly against serotypes of *S. pneumoniae* whose polysaccharides are not
- 20 incorporated in the existing vaccine formulations.

The vaccine is preferably administered by sub-cutaneous injection, with or without an approved adjuvant, such as alumina gel.

- 25 In another form the invention could be said to reside in a recombinant clone including a replicon and a DNA sequence encoding an altered pneumolysin, said altered pneumolysin being non-toxic and being capable of eliciting an immune response in an animal being reactive to wild-type pneumolysin.

- 30 In yet another form the invention could be said to reside in a method of producing an altered pneumolysin including the steps of purifying said altered pneumolysin from an expression system including a recombinant clone with DNA encoding an altered pneumolysin said
- 35 pneumolysin being substantially non-toxic and being capable of eliciting an immune response in an animal reactive to wild-type pneumolysin.

Preferrably the expression system is a culture of a host cell including a recombinant clone with DNA encoding the altered pneumolysin.

5 In another form the invention could be said to reside in a method of producing a vaccine including the step of amplifying a recombinant clone encoding an altered pneumolysin, inducing transcription and translation of said cloned material, the purification of altered pneumolysin, and the step of conjugating the altered pneumolysin with a capsular polysaccharide, the altered pneumolysin having
10 substantially reduced toxic activity as compared with wild-type pneumolysin.

15 For a better understanding of the invention specific embodiments of the invention will now be described with reference to diagrams wherein:-

FIG. 1 Is the DNA sequence of the gene encoding wild-type pneumolysin,

20 FIG. 2 Is the DNA sequence of an altered gene encoding wild type pneumolysin used for cloning the pneumolysin gene into an expression vector,

25 FIG. 3 Is the amino acid sequence of the wild-type pneumolysin as derived from the DNA sequence of the gene encoding the wild type pneumolysin, and

FIG. 4 shows the amino acid sequence of pneumolysin showing amino acid substitutions introduced by site directed mutagenesis.
30

Recombinant DNA techniques have been used to construct non-toxic pneumolysin derivatives suitable for administration to humans. To achieve this, the *S. pneumoniae* gene encoding pneumolysin was
35 cloned into *Escherichia coli* and its complete DNA sequence determined. The DNA sequence is shown in Figure 1 and the derived amino acid sequence is shown in Figure 3.

Three regions of the pneumolysin gene were subjected to oligonucleotide-directed mutagenesis. The first region encodes amino acids 427 - 437 in the protein sequence, and is indicated by an underline in Figure 3. This 11 amino acid sequence shows absolute
5 homology with similar regions in other related thiol activated toxins thus is thought to be responsible for the haemolytic activity and hence toxic activity of the toxin. The other two regions encode amino acids 257 - 297 and amino acids 368 - 397 and are also indicated by an underline in Figure 3. These two regions of the toxin have substantial
10 amino acid sequence homology with human C-reactive protein (CRP), and by inference therefore, are thought to be responsible for the ability of pneumolysin to bind the Fc region of immunoglobulins and to activate complement. Fifteen separate mutations in the pneumolysin gene, resulting in single amino acid substitutions, were constructed, as
15 shown in Figure 4. In an effort to maintain the structure of the altered pneumolysin, conservative substitutions were made, so that amino acids are substituted with amino acids of a similar nature.

For the region involved in haemolytic activity, Cys 428 -> Gly, Cys 428 -> Ser, Trp₄₃₃ -> Phe, Glu₄₃₄ -> Asp and Trp₄₃₅ -> Phe each reduced
20 haemolytic activity by 97%, 90%, 99%, 75% and 90% respectively. The other mutations in that region (Cys₄₂₈ -> Ala, Glu₄₃₄ -> Gln and Trp 436 ->Phe) did not affect haemolytic activity. Mutating a separate region of the toxin thought to be responsible for binding to target cell membranes
25 also affects haemolytic activity of the protein. This substitution, His₃₆₇ -> Arg, completely inhibits haemolytic activity. This is a quite unpredictable finding in that His₃₆₇ -> Arg therefore shows a greater inhibition of this property than the substitutions made within the 11 amino acid region thought to be responsible for haemolytic activity.
30

Mutations in the CRP-like domains were tested for ability to activate complement. For Trp₃₇₉ -> Phe, Tyr₃₈₄ -> Phe, Asp₃₈₅ -> Asn, and Trp₃₉₇ -> Phe, complement activation was reduced by 20%, 70%, 100% and 15%, respectively. The other mutations in the CRP-like
35 domains shown in Figure 4 do not reduce complement activation.

Importantly, the above mutations which affect either haemolytic activity or complement activation do not impair the immunogenicity of the proteins, compared with native or wild-type pneumolysin.

- 5 Thus although His₃₆₇ → Arg is the preferred mutation to reduce the haemolytic activity, a combination of two or more mutants effecting reduced haemolytic activity can also achieve a very high level of reduction in haemolytic activity. Similarly Asp₃₈₅ → Asn is the preferred mutation to achieve reduced complement activation, however a
10 combination of two or more other mutants that reduce the activity to a lesser degree can also be used.

In a preferred embodiment the pneumolysin derivative for use in the vaccine would contain a combination of certain of the above mutations
15 such that the protein is unable to activate complement in addition to having zero haemolytic activity. Examples of such combination are:-

- 1) His₃₆₇ → Arg + Asp₃₈₅ → Asn,
- 2) His₃₆₇ → Arg + Asp₃₈₅ → Asn + either Cys₄₂₈ → Gly or Trp₄₃₃ → Phe
- 20 3) Asp₃₈₅ → Asn + Cys₄₂₈ → Gly + Trp₄₃₃ → Phe

These then are some preferred combinations, however it is to be understood that other combinations of mutations can be used to make up the altered pneumolysin for use in a vaccine. Further the altered
25 pneumolysin may comprise any one of the individual mutations with sufficiently reduced activity.

High level expression of the altered pneumolysin from DNA encoding the altered pneumolysin can be achieved by using any one of a number
30 of conventional techniques including the expression in a prokaryotic host with the DNA cloned appropriately within any one of the many expression vectors currently available, or cloned appropriately within the host chromosome; expression in a eukaryotic host with the DNA cloned appropriately either within an expression vector or cloned within
35 the host chromosome; or within an *in vitro* expression system such as may comprise purified components necessary for expression of altered pneumolysin.

To achieve high level expression of the mutated pneumolysin gene, it has been cloned into the vector pKK233-2 for expression within *Escherichia coli* or other like prokaryote. This vector included ampicillin and tetracycline resistance genes, the *trc* promoter (which can be regulated by IPTG [isopropyl- β -D-thiogalactopyranoside]), and a *lac Z* ribosome binding site adjacent to an ATG initiation codon incorporating an *NcoI* restriction site. Immediately downstream from the initiation codon there are restriction sites for *PstI* and *HindIII*, followed by a strong $T_1 T_2$ transcription terminator. Prior to insertion into pKK233-2, a *NcoI* restriction site was constructed at the 5' end of the pneumolysin coding sequence (at the initiation codon) by oligonucleotide-directed mutagenesis, as shown in Figure 2. This enabled the proximal end of the altered pneumolysin gene to be cloned into the *NcoI* site of pKK233-2; a *HindIII* site approximately 80 bases downstream from the pneumolysin termination codon was used to splice the distal end of the altered gene into the compatible site in pKK233-2. The mutant pneumolysin derivative could however, be cloned into any one of a number of high expression vector systems.

The mutant pneumolysin is prepared as follows: *E. coli* cells harbouring the above recombinant plasmid are first grown in 9 litre cultures in Luria Bertani (or any other appropriate) medium, supplemented with the appropriate antibiotic, at 37° C, with aeration. When the culture reaches the late logarithmic phase of growth, IPTG is added to a final concentration of 20 μ M (to induce expression of the altered pneumolysin gene) and incubation is continued for a further 2 to 3 hours.

Cells are then harvested by centrifugation or ultrafiltration and lysed by treatment with EDTA and lysozyme, followed by sonication, or by disruption in a French pressure cell. Cell debris is removed by centrifugation and the extract is then dialysed extensively against 10mM sodium phosphate (pH7.0). The material is then loaded onto a column of DEAE-cellulose and eluted with a linear gradient of 10-250mM sodium phosphate (pH7.0). Fractions containing peak levels of the pneumolysin derivative are pooled, concentrated by ultrafiltration and loaded onto a column of Sephacryl S-200. This column is developed in 50mM sodium phosphate (pH7.0) and again fractions with high levels of pneumolysin derivative are pooled, concentrated by

ultrafiltration and stored in 50% glycerol at -15°C. The final product is greater than 95% pure, as judged by SDS-polyacrylamide gel electrophoresis. Hydrophobic interaction chromatography on Phenyl-Sepharose is an alternative purification which could also be used.

- 5 However it is to be understood that this is only one method of purification of the altered pneumolysin, and other, alternative methods (including High Pressure Liquid Chromatography) may be employed.

- 10 This purified altered pneumolysin can then be administered as a vaccine at appropriate levels, either by itself or in combination with other antigens. In one form the pneumolysin may be conjugated with polysaccharide derived from any one or more of the variety of pneumococcal strains described above.

- 15 The mutant pneumolysin can be conjugated to the various serotypes of polysaccharide by a range of methods. The first involves preparation of an activated polysaccharide by treating pure polysaccharide (available commercially) with cyanogen-bromide and adipicacid dihydrazide (ADH). The ADH-polysaccharide is then combined with the mutant
20 pneumolysin in the presence of 1-ethyl-3-(3-dimethylaminopropyl) carbodiimide - HCl. Conjugated material is separated from the reactants by chromatography through Sepharose CL-4B.

- Alternatively, the polysaccharide-mutant pneumolysin conjugates can
25 be prepared using bifunctional reagents such as N-succinimidyl-6(4'-azido-2'-nitrophenylamino)hexanoate (SANPAH). Pure polysaccharide dissolved in phosphate buffered saline, is reacted with SANPAH in the presence of a strong white light source. Unreacted SANPAH is then separated from activated polysaccharide by chromatography on
30 Sephadex G-50. Activated polysaccharide is then conjugated to the mutant pneumolysin in 0.2M borate buffer (pH8.5). Any excess reactive groups are then blocked with lysine, and the polysaccharide-protein conjugate is separated from the other reactants by chromatography on Sepharose CL-4B. Conjugates could also be prepared by reductive
35 amination with cyanoborohydride.

Alternatively another protein, such as inactivated tetanus toxin, can be conjugated with the desired polysaccharides and altered pneumolysin can be added to the vaccine in an unconjugated form.

5

This then describes the best method of performing the invention however it is to be understood that the invention is not limited thereto.

1. An altered pneumolysin being substantially non-toxic and being capable of eliciting an immune response in an animal being reactive to wild-type pneumolysin.
- 5 2. An altered pneumolysin as in claim one having reduced complement binding activity as compared to wild-type pneumolysin.
3. An altered pneumolysin as in any one of claims 1 or 2 having reduced Fc binding activity as compared to wild-type pneumolysin.
- 10 4. An altered pneumolysin as in any one of claims 1, 2, or 3 wherein said altered pneumolysin is altered by reason of one or more amino acid substitutions within wild type pneumolysin.
- 15 5. An altered pneumolysin having the following amino acid sequence:-

1	Met	Ala	Asn	Lys	Ala	Val	Asn	Asp	Phe	Ile	Leu	Ala	Met
											11		
20	Asn	Tyr	Asp	Lys	Lys	Lys	Leu	Leu	Thr	His	Gln	Gly	Glu
								21					
	Ser	Ile	Glu	Asn	Arg	Phe	Ile	Lys	Glu	Gly	Asn	Gln	Leu
					31								
	Pro	Asp	Glu	Phe	Val	Val	Ile	Glu	Arg	Lys	Lys	Arg	Ser
		41										51	
25	Leu	Ser	Thr	Asn	Thr	Ser	Asp	Ile	Ser	Val	Thr	Ala	Thr
									61				
	Asn	Asp	Ser	Arg	Leu	Tyr	Pro	Gly	Ala	Leu	Leu	Val	Val
						71							
	Asp	Glu	Thr	Leu	Leu	Glu	Asn	Asn	Pro	Thr	Leu	Leu	Ala
30			81										91
	Val	Asp	Arg	Ala	Pro	Met	Thr	Tyr	Ser	Ile	Asp	Leu	Pro
										101			
	Gly	Leu	Ala	Ser	Ser	Asp	Ser	Phe	Leu	Gln	Val	Glu	Asp
							111						
35	Pro	Ser	Asn	Ser	Ser	Val	Arg	Gly	Ala	Val	Asn	Asp	Leu
			121										
	Leu	Ala	Lys	Trp	His	Gln	Asp	Tyr	Gly	Gln	Val	Asn	Asn
											141		
	Val	Pro	Ala	Arg	Met	Gln	Tyr	Glu	Lys	Ile	Thr	Ala	His
40								151					
	Ser	Met	Glu	Gln	Leu	Lys	Val	Lys	Phe	Gly	Ser	Asp	Phe
					161								
	Glu	Lys	Thr	Gly	Asn	Ser	Leu	Asp	Ile	Asp	Phe	Asn	Ser
		171										181	
45	Val	His	Ser	Gly	Glu	Lys	Gln	Ile	Gln	Ile	Val	Asn	Phe
									191				

	Lys	Gln	Ile	Tyr	Tyr	Thr	Val	Ser	Val	Asp	Ala	Val	Lys
	Asn	Pro	Gly	Asp	Val	Phe	Gln	Asp	Thr	Val	Thr	Val	Glu
5	Asp	Leu	Lys	Gln	Arg	Gly	Ile	Ser	Ala	Glu	Arg	Pro	Leu
	Val	Tyr	Ile	Ser	Ser	Val	Ala	Tyr	Gly	Arg	Gln	Val	Tyr
10	Leu	Lys	Leu	Glu	Thr	Thr	Ser	Lys	Ser	Asp	Glu	Val	Glu
	Ala	Ala	Phe	Glu	Ala	Leu	Ile	Lys	Gly	Val	Lys	Val	Ala
15	Pro	Gln	Thr	Glu	Trp	Lys	Gln	Ile	Leu	Asp	Asn	Thr	Glu
	Val	Lys	Ala	Val	Ile	Leu	Gly	Gly	Asp	Pro	Ser	Ser	Gly
	Ala	Arg	Val	Val	Thr	Gly	Lys	Val	Asp	Met	Val	Glu	Asp
20	Leu	Ile	Gln	Glu	Gly	Ser	Arg	Phe	Thr	Ala	Asp	His	Pro
	Gly	Leu	Pro	Ile	Ser	Tyr	Thr	Thr	Ser	Phe	Leu	Arg	Asp
25	Asn	Val	Val	Ala	Thr	Phe	Gln	Asn	Ser	Thr	Asp	Tyr	Val
	Glu	Thr	Lys	Val	Thr	Ala	Tyr	Arg	Asn	Gly	Asp	Leu	Leu
	Leu	Asp	R ₁	Ser	Gly	Ala	Tyr	Val	Ala	Gln	Tyr	Tyr	Ile
30	Thr	R ₂	Asp	Glu	Leu	Ser	R ₃	R ₄	His	Gln	Gly	Lys	Glu
	Val	Leu	Thr	Pro	Lys	Ala	R ₅	Asp	Arg	Asn	Gly	Gln	Asp
35	Leu	Thr	Ala	His	Phe	Thr	Thr	Ser	Ile	Pro	Leu	Lys	Gly
	Asn	Val	Arg	Asn	Leu	Ser	Val	Lys	Ile	Arg	Glu	R ₆	Thr
	Gly	Leu	Ala	R ₇	R ₈	R ₉	Trp	Arg	Thr	Val	Tyr	Glu	Lys
40	Thr	Asp	Leu	Pro	Leu	Val	Arg	Lys	Arg	Thr	Ile	Ser	Ile
	Trp	Gly	Thr	Thr	Leu	Tyr	Pro	Gln	Val	Glu	Asp	Lys	Val
45	Glu	Asn	Asp										

wherein R₁ is His or Arg, R₂ is Trp or Phe, R₃ is Tyr or Phe, R₄ is Asp or Asn, R₅ is Trp or Phe, R₆ is Cys, Gly, or Ser, R₇ is Trp or Phe, R₈ is Glu, or Asp, R₉ is Trp or Phe, and wherein at least one of the residues R₁, R₆, R₇, R₈, or R₉ is other than wild-type.

6. An altered pneumolysin as in claim 5 wherein wherein R₁ is Arg, R₂ is Trp, R₃ is Tyr, R₄ is Asn, R₅ is Trp, R₆ is Cys, R₇ is Trp, R₈ is Glu, and R₉ is Trp.
- 5 7. A vaccine including an altered pneumolysin, said altered pneumolysin being non-toxic and being capable of eliciting an immune response in an animal being reactive to wild-type pneumolysin.
8. A vaccine as in claim 7 wherein the altered pneumolysin is as
10 claimed in any one of claims 2 to 6.
9. A vaccine comprising capsular polysaccharide material conjugated with a protein carrier and non-conjugated protein material, the capsular polysaccharide material being derived from any one or
15 more than one of the *Streptococcus pneumoniae* serotypes, and the non-conjugated protein material being an altered pneumolysin, said altered pneumolysin being non-toxic and being capable of eliciting an immune response in an animal reactive to wild type pneumolysin.
- 20 10. A vaccine as in claim 9 wherein the capsular material is derived from any one or more of the *Streptococcus pneumoniae* serotypes 6A, 6B, 14, 18C, 19A, 19F, 23F, 1, 2, 3, 4, 5, 7F, 8, 9N, 9V, 10A, 11A, 12F, 15B, 17F, 20, 22F and 33F.
- 25 11. A vaccine as in either claim 9 or 10 wherein the altered pneumolysin is as claimed in as in any one of claims 2 to 6.
12. A vaccine comprising capsular polysaccharide material conjugated with a protein carrier, the capsular polysaccharide material
30 being derived from any one or more than one of the *Streptococcus pneumoniae* serotypes, and the protein carrier being an altered pneumolysin, said altered pneumolysin being non-toxic and being capable of eliciting an immune response in an animal reactive to wild type pneumolysin.
- 35 13. A vaccine as in claim 12 wherein the capsular material is derived from any one or more of the *Streptococcus pneumoniae* serotypes 6A,

6B, 14, 18C, 19A, 19F, 23F, 1, 2, 3, 4, 5, 7F, 8, 9N, 9V, 10A, 11A, 12F, 15B, 17F, 20, 22F and 33F.

14. A vaccine as in either claim 12 or 13 wherein the altered pneumolysin is as claimed in any one of claims 2 to 6.
15. A recombinant plasmid including a DNA sequence encoding an altered pneumolysin as claimed in any one of claims 1 to 6.
16. A hybrid host cell including a recombinant plasmid as claimed in claim 9 said recombinant plasmid including an inducible expression control operable for expression of said altered pneumolysin encoding DNA within a host cell.
17. A method of producing an altered pneumolysin including the steps of purifying said altered pneumolysin from an expression system including a recombinant plasmid with DNA encoding an altered pneumolysin said pneumolysin being substantially non-toxic and being capable of eliciting an immune response in an animal reactive to wild type pneumolysin.
18. A method of producing an altered pneumolysin including the steps of purifying said altered pneumolysin from a culture of a host cell including a recombinant clone with DNA encoding an altered pneumolysin said pneumolysin being substantially non-toxic and being capable of eliciting an immune response in an animal said immune response being reactive to wild type pneumolysin.
19. A method of producing a vaccine including the step of amplifying a recombinant clone encoding an altered pneumolysin, inducing transcription and translation of said cloned material, the purification of altered pneumolysin, and the step of conjugating the altered pneumolysin with a capsular polysaccharide, the altered pneumolysin having substantially reduced toxic activity as compared with wild type pneumolysin.
20. A method of producing a vaccine as in claim 19 wherein said altered pneumolysin is as claimed in any one of claims 2 to 6.

21. An altered pneumolysin as hereinbefore described with reference to the examples.

5 22. A vaccine including an altered pneumolysin as hereinbefore described with reference to the examples.

23. A method of producing a vaccine as hereinbefore described with reference to the examples.

AGATGGCAAA TAAAGCAGTA AATGACTTTA TACTAGCTAT GAATTACGAT
AAAAAGAAAC TCTTGACCCA TCAGGGAGAA AGTATTGAAA ATCGTTTCAT
CAAAGAGGGT AATCAGCTAC CCGATGAGTT TGTTGTTATC GAAAGAAAGA
AGCGGAGCTT GTCGACAAAT ACAAGTGATA TTTCTGTAAC AGCTACCAAC
GACAGTCGCC TCTATCCTGG AGCACTTCTC GTAGTGGATG AGACCTTGTT
AGAGAATAAT CCCACTCTTC TTGCGGTTGA TCGTGCTCCG ATGACTTATA
GTATTGATTT GCCTGGTTTG GCAAGTAGCG ATAGCTTTCT CCAAGTGGAA
GACCCCAGCA ATTCAAGTGT TCGCGGAGCG GTAAACGATT TGTTGGCTAA
GTGGCATCAA GATTATGGTC AGGTCAATAA TGTCCCAGCT AGAATGCAGT
ATGAAAAAAT AACGGCTCAC AGCATGGAAC AACTCAAGGT CAAGTTTGGT
TCTGACTTTG AAAAGACAGG GAATTCTCTT GATATTGATT TTA ACTCTGT
CCATTCAGGT GAAAAGCAGA TTCAGATTGT TAATTTTAAG CAGATTTATT
ATACAGTCAG CGTAGACGCT GTTAAAAATC CAGGAGATGT GTTTC AAGAT
ACTGTAACGG TAGAGGATTT AAAACAGAGA GGAATTTCTG CAGAGCGTCC
TTTGGTCTAT ATTTGAGTG TTGCTTATGG GCGCCAAGTC TATCTCAAGT
TGGA AACCAC GAGTAAGAGT GATGAAGTAG AGGCTGCTTT TGAAGCTTTG
ATAAAAGGAG TCAAGGTAGC TCCTCAGACA GAGTGGAAGC AGATTTTGGA
CAATACAGAA GTGAAGGCGG TTATTTTAGG GGGCGACCCA AGTTCGGGTG
CCCGAGTTGT AACAGGCAAG GTGGATATGG TAGAGGACTT GATTCAAGAA
GGCAGTCGCT TTACAGCAGA TCATCCAGGC TTGCCGATTT CCTATACAAC
TTCTTTTTTA CGTGACAATG TAGTTGCGAC CTTTCAAAAC AGTACAGACT
ATGTTGAGAC TAAGGTTACA GCTTACAGAA ACGGAGATTT ACTGCTGGAT
CATAGTGGTG CCTATGTTGC CCAATATTAT ATTACTTGGG ATGAATTATC
CTATGATCAT CAAGGTAAGG AAGTCTTGAC TCCTAAGGCT TGGGACAGAA
ATGGGCAGGA TTTGACGGCT CACTTTACCA CTAGTATTCC TTTAAAAGGG
AATGTTGTA ATCTCTCTGT CAAAATTAGA GAGTGTACCG GGCTTGCCTG
GGAATGGTGG CGTACGGTTT ATGAAAAAAC CGATTTGCCA CTAGTGCCTA
AGCGGACGAT TTCTATTTGG GGAACAAC TC TATCCTCA GGTAGAGGAT
AAGGTAGAAA ATGAC

FIGURE 1 DNA sequence of pneumolysin gene. ATG start codon underlined

CCATGGCAAA TAAAGCAGTA AATGACTTTA TACTAGCTAT GAATTACGAT
AAAAAGAAAC TCTTGACCCA TCAGGGAGAA AGTATTGAAA ATCGTTTCAT
CAAAGAGGGT AATCAGCTAC CCGATGAGTT TGTGTTATC GAAAGAAAGA
AGCGGAGCTT GTCGACAAAT ACAAGTGATA TTTCTGTAAC AGCTACCAAC
GACAGTCGCC TCTATCCTGG AGCACTTCTC GTAGTGGATG AGACCTTGTT
AGAGAATAAT CCCACTCTTC TTGCGGTTGA TCGTGCTCCG ATGACTTATA
GTATTGATTT GCCTGGTTTG GCAAGTAGCG ATAGCTTTCT CCAAGTGGAA
GACCCAGCA ATTCAAGTGT TCGCGGAGCG GTAAACGATT TGTTGGCTAA
GTGGCATCAA GATTATGGTC AGGTCAATAA TGTCCCAGCT AGAATGCAGT
ATGAAAAAAT AACGGCTCAC AGCATGGAAC AACTCAAGGT CAAGTTTGGT
TCTGACTTTG AAAAGACAGG GAATTCTCTT GATATTGATT TTAAGTCTGT
CCATTCAGGT GAAAAGCAGA TTCAGATTGT TAATTTTAAG CAGATTTATT
ATACAGTCAG CGTAGACGCT GTTAAAAATC CAGGAGATGT GTTCAAGAT
ACTGTAACGG TAGAGGATTT AAAACAGAGA GGAATTTCTG CAGAGCGTCC
TTTGGTCTAT ATTTGAGTG TTGCTTATGG GCGCCAAGTC TATCTCAAGT
TGGAACCAC GAGTAAGAGT GATGAAGTAG AGGCTGCTTT TGAAGCTTTG
ATAAAGGAG TCAAGGTAGC TCCTCAGACA GAGTGAAGC AGATTTTGGA
CAATACAGAA GTGAAGGCGG TTATTTTAGG GGGCGACCCA AGTTCGGGTG
CCCGAGTTGT AACAGGCAAG GTGGATATGG TAGAGGACTT GATTCAAGAA
GGCAGTCGCT TTACAGCAGA TCATCCAGGC TTGCCGATTT CCTATACAAC
TTCTTTTTTA CGTGACAATG TAGTTGCGAC CTTTCAAAC AGTACAGACT
ATGTTGAGAC TAAGGTTACA GCTTACAGAA ACGGAGATTT ACTGCTGGAT
CATAGTGGTG CCTATGTTGC CCAATATTAT ATTACTTGGG ATGAATTATC
CTATGATCAT CAAGGTAAGG AAGTCTTGAC TCCTAAGGCT TGGGACAGAA
ATGGGCAGGA TTTGACGGCT CACTTTACCA CTAGTATTCC TTTAAAGGG
AATGTTGTA ATCTCTCTGT CAAATTAGA GAGTGACCG GGCTTGCCTG
GGAATGGTGG CGTACGGTTT ATGAAAAAAC CGATTTGCCA CTAGTGCCTA
AGCGGACGAT TTCTATTTGG GGAACAACTC TCTATCCTCA GGTAGAGGAT
AAGGTAGAAA ATGAC

FIGURE 2 DNA sequence of modified pneumolysin gene.
An NcoI restriction site (underlined) has
been introduced at the start codon

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Met Ala Asn Lys Ala Val Asn Asp Phe Ile Leu Ala Met
 1 11
 Asn Tyr Asp Lys Lys Lys Leu Leu Thr His Gln Gly Glu
 21
 Ser Ile Glu Asn Arg Phe Ile Lys Glu Gly Asn Gln Leu
 31
 Pro Asp Glu Phe Val Val Ile Glu Arg Lys Lys Arg Ser
 41 51
 Leu Ser Thr Asn Thr Ser Asp Ile Ser Val Thr Ala Thr
 61
 Asn Asp Ser Arg Leu Tyr Pro Gly Ala Leu Leu Val Val
 71
 Asp Glu Thr Leu Leu Glu Asn Asn Pro Thr Leu Leu Ala
 81 91
 Val Asp Arg Ala Pro Met Thr Tyr Ser Ile Asp Leu Pro
 101
 Gly Leu Ala Ser Ser Asp Ser Phe Leu Gln Val Glu Asp
 111
 Pro Ser Asn Ser Ser Val Arg Gly Ala Val Asn Asp Leu
 121
 Leu Ala Lys Trp His Gln Asp Tyr Gly Gln Val Asn Asn
 131 141
 Val Pro Ala Arg Met Gln Tyr Glu Lys Ile Thr Ala His
 151
 Ser Met Glu Gln Leu Lys Val Lys Phe Gly Ser Asp Phe
 161
 Glu Lys Thr Gly Asn Ser Leu Asp Ile Asp Phe Asn Ser
 171 181
 Val His Ser Gly Glu Lys Gln Ile Gln Ile Val Asn Phe
 191
 Lys Gln Ile Tyr Tyr Thr Val Ser Val Asp Ala Val Lys
 201
 Asn Pro Gly Asp Val Phe Gln Asp Thr Val Thr Val Glu
 211 221

Asp Leu Lys Gln Arg Gly Ile Ser Ala Glu Arg Pro Leu
 231
 Val Tyr Ile Ser Ser Val Ala Tyr Gly Arg Gln Val Tyr
 241
 Leu Lys Leu Glu Thr Thr Ser Lys Ser Asp Glu Val Glu
 251
 Ala Ala Phe Glu Ala Leu Ile Lys Gly Val Lys Val Ala
 261 271
 Pro Gln Thr Glu Trp Lys Gln Ile Leu Asp Asn Thr Glu
 281
Val Lys Ala Val Ile Leu Gly Gly Asp Pro Ser Ser Gly
 291
 Ala Arg Val Val Thr Gly Lys Val Asp Met Val Glu Asp
 301 311
 Leu Ile Gln Glu Gly Ser Arg Phe Thr Ala Asp His Pro
 321
 Gly Leu Pro Ile Ser Tyr Thr Thr Ser Phe Leu Arg Asp
 331
 Asn Val Val Ala Thr Phe Gln Asn Ser Thr Asp Tyr Val
 341 351
 Glu Thr Lys Val Thr Ala Tyr Arg Asn Gly Asp Leu Leu
 361
 Leu Asp His Ser Gly Ala Tyr Val Ala Gln Tyr Tyr Ile
 371
Thr Trp Asp Glu Leu Ser Tyr Asp His Gln Gly Lys Glu
 381
Val Leu Thr Pro Lys Ala Trp Asp Arg Asn Gly Gln Asp
 391 401
 Leu Thr Ala His Phe Thr Thr Ser Ile Pro Leu Lys Gly
 411
 Asn Val Arg Asn Leu Ser Val Lys Ile Arg Glu Cys Thr
 421
Gly Leu Ala Trp Glu Trp Trp Arg Thr Val Tyr Glu Lys
 431 441
 Thr Asp Leu Pro Leu Val Arg Lys Arg Thr Ile Ser Ile
 451

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Trp Gly Thr Thr Leu Tyr Pro Gln Val Glu Asp Lys Val
461

Glu Asn Asp
471

Figure 3

Met	Ala	Asn	Lys	Ala	Val	Asn	Asp	Phe	Ile	Leu	Ala	Met
1										11		
Asn	Tyr	Asp	Lys	Lys	Lys	Leu	Leu	Thr	His	Gln	Gly	Glu
						21						
Ser	Ile	Glu	Asn	Arg	Phe	Ile	Lys	Glu	Gly	Asn	Gln	Leu
			31									
Pro	Asp	Glu	Phe	Val	Val	Ile	Glu	Arg	Lys	Lys	Arg	Ser
	41										51	
Leu	Ser	Thr	Asn	Thr	Ser	Asp	Ile	Ser	Val	Thr	Ala	Thr
								61				
Asn	Asp	Ser	Arg	Leu	Tyr	Pro	Gly	Ala	Leu	Leu	Val	Val
					71							
Asp	Glu	Thr	Leu	Leu	Glu	Asn	Asn	Pro	Thr	Leu	Leu	Ala
		81										91
Val	Asp	Arg	Ala	Pro	Met	Thr	Tyr	Ser	Ile	Asp	Leu	Pro
									101			
Gly	Leu	Ala	Ser	Ser	Asp	Ser	Phe	Leu	Gln	Val	Glu	Asp
						111						
Pro	Ser	Asn	Ser	Ser	Val	Arg	Gly	Ala	Val	Asn	Asp	Leu
			121									
Leu	Ala	Lys	Trp	His	Gln	Asp	Tyr	Gly	Gln	Val	Asn	Asn
	131									141		
Val	Pro	Ala	Arg	Met	Gln	Tyr	Glu	Lys	Ile	Thr	Ala	His
							151					
Ser	Met	Glu	Gln	Leu	Lys	Val	Lys	Phe	Gly	Ser	Asp	Phe
				161								
Glu	Lys	Thr	Gly	Asn	Ser	Leu	Asp	Ile	Asp	Phe	Asn	Ser
	171										181	
Val	His	Ser	Gly	Glu	Lys	Gln	Ile	Gln	Ile	Val	Asn	Phe
								191				
Lys	Gln	Ile	Tyr	Tyr	Thr	Val	Ser	Val	Asp	Ala	Val	Lys
					201							
Asn	Pro	Gly	Asp	Val	Phe	Gln	Asp	Thr	Val	Thr	Val	Glu
		211										221
Asp	Leu	Lys	Gln	Arg	Gly	Ile	Ser	Ala	Glu	Arg	Pro	Leu
									231			

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Val	Tyr	Ile	Ser	Ser	Val	Ala	Tyr	Gly	Arg	Gln	Val	Tyr
						241						
Leu	Lys	Leu	Glu	Thr	Thr	Ser	Lys	Ser	Asp	Glu	Val	Glu
			251									
		Trp										
Ala	Ala	Phe	Glu	Ala	Leu	Ile	Lys	Gly	Val	Lys	Val	Ala
261										271		
				Phe								
Pro	Gln	Thr	Glu	Trp	Lys	Gln	Ile	Leu	Asp	Asn	Thr	Glu
							281					
Val	Lys	Ala	Val	Ile	Leu	Gly	Gly	Asp	Pro	Ser	Ser	Gly
				291								
Ala	Arg	Val	Val	Thr	Gly	Lys	Val	Asp	Met	Val	Glu	Asp
	301										311	
Leu	Ile	Gln	Glu	Gly	Ser	Arg	Phe	Thr	Ala	Asp	His	Pro
								321				
Gly	Leu	Pro	Ile	Ser	Tyr	Thr	Thr	Ser	Phe	Leu	Arg	Asp
					331							
Asn	Val	Val	Ala	Thr	Phe	Gln	Asn	Ser	Thr	Asp	Tyr	Val
		341										351
Glu	Thr	Lys	Val	Thr	Ala	Tyr	Arg	Asn	Gly	Asp	Leu	Leu
									361			
		Arg										
Leu	Asp	His	Ser	Gly	Ala	Tyr	Val	Ala	Gln	Tyr	Tyr	Ile
						371						
	Phe						Phe	Asn				
Thr	Trp	Asp	Glu	Leu	Ser	Tyr	Asp	His	Gln	Gly	Lys	Glu
			381									
							Phe					
Val	Leu	Thr	Pro	Lys	Ala	Trp	Asp	Arg	Asn	Gly	Gln	Asp
391										401		
Leu	Thr	Ala	His	Phe	Thr	Thr	Ser	Ile	Pro	Leu	Lys	Gly
							411					

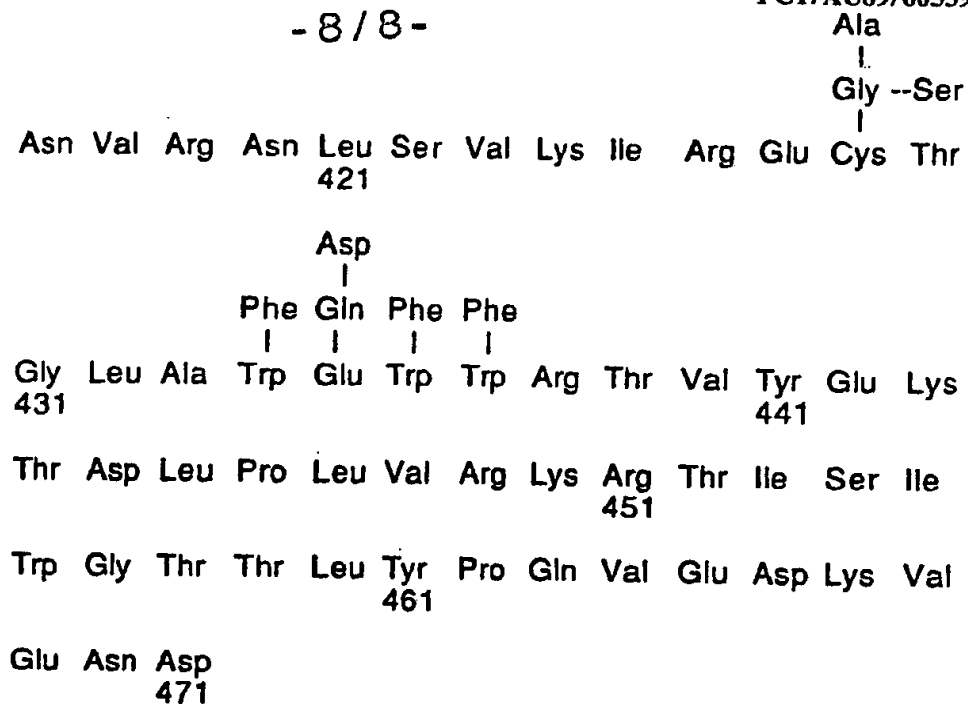
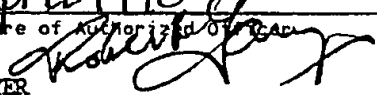


Figure 4

INTERNATIONAL SEARCH REPORT

International Application No. PCT/AU 89/00539

I. CLASSIFICATION OF SUBJECT MATTER (if several classification symbols apply, indicate all) 6		
According to International Patent Classification (IPC) or to both National Classification and IPC Int.Cl. ⁵ C07K 13/00, C12P 21/00, C12N 15/31, C07H 21/04		
II. FIELDS SEARCHED		
Minimum Documentation Searched 7		
Classification System	Classification Symbols	
IPC	Derwent databases: WPI, WPIL, USPA; keywords STREPTOCOCCUS PNEUMONIAE, PNEUMOCOCCUS, PNEUMOLYSIN HAEMOLYSIN, HEMOLYSIN, CBR, COMPLEMENT BINDING REGION CPR, REACTIVE PROTEIN	
Documentation Searched other than Minimum Documentation to the Extent that such Documents are Included in the Fields Searched 8		
Aust Class: C07K 13/00, 15/04 C12N 15/31 CHEM ABS using keywords above		
III. DOCUMENTS CONSIDERED TO BE RELEVANT 9		
Category*	Citation of Document, ¹¹ with indication, where appropriate, of the relevant passages 12	Relevant to Claim No 13
PX	Infection and Immunity, Vol 57 (8) Aug 1989 p2547-2552 F.K. SAUNDERS et al "Pneumolysin, the Thiol-Activated Toxin of <u>Streptococcus pneumoniae</u> , does not require a Thiol Group for In Vitro Activity"	1, 4-5, 15-21
A	Infection and Immunity, Vol 55 (5) May 1987, p1184-1189 WALKER, J.A. et al "Molecular Cloning, Characterization, and complete Nucleotide Sequence of the Gene for Pneumolysin, the Sulfhydryl-Activated Toxin of <u>Streptococcus pneumoniae</u>	1-22
A	Journal of Clinical Microbiology Feb 1987 p222-225 Krzysztof Kancierski et al "Production and Purification of <u>Streptococcus pneumoniae</u> Hemolysin (Pneumolysin)	1-22
* Special categories of cited documents: 10		
"A" document defining the general state of the art which is not considered to be of particular relevance	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention	
"E" earlier document but published on or after the international filing date	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step	
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.	
"O" document referring to an oral disclosure, use, exhibition or other means	"G" document member of the same patent family	
"P" document published prior to the international filing date but later than the priority date claimed		
IV. CERTIFICATION		
Date of the Actual Completion of the International Search 6 April 1990 (06.04.90)	Date of Mailing of this International Search Report 12 April 1990	
International Searching Authority Australian Patent Office	Signature of Authorized Official  R. SAWYER	